



16001  
Raw Seq 03/18/2002  
7/31/03

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/647,522

DATE: 03/18/2002  
TIME: 15:20:39

Input Set : A:\Nagai.h.app  
Output Set: N:\CRF3\03182002\I647522.raw

3 <110> APPLICANT: NAGAI, Hiroshi  
4 NAKAJIMA, Terumi  
6 <120> TITLE OF INVENTION: NOVEL HEMOLYTIC ACTIVE PROTEINS AND GENES ENCODING THE  
7 SAME  
9 <130> FILE REFERENCE: PCTJP9901607NAGAIHiroshietal 183049264  
11 <140> CURRENT APPLICATION NUMBER: US/09/647,522  
12 <141> CURRENT FILING DATE: 2000-10-02  
14 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01607  
15 <151> PRIOR FILING DATE: 1999-03-30  
17 <150> PRIOR APPLICATION NUMBER: JP 10/88569  
18 <151> PRIOR FILING DATE: 1998-04-01  
20 <160> NUMBER OF SEQ ID NOS: 18  
22 <170> SOFTWARE: PatentIn Ver. 2.0  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 14  
26 <212> TYPE: PRT  
27 <213> ORGANISM: Carybdea rastonii  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: This amino acid residue sequence corresponds to  
31 amino acid residue positions 56-69 of SEQ ID NO:5.  
33 <400> SEQUENCE: 1  
34 Gly Glu Ile Gln Thr Lys Pro Asp Arg Val Gly Gln Ala Thr  
35 1 5 10  
38 <210> SEQ ID NO: 2  
39 <211> LENGTH: 18  
40 <212> TYPE: PRT  
41 <213> ORGANISM: Carybdea rastonii  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: This amino acid residue sequence corresponds to  
45 amino acid residue positions 250-267 of SEQ ID  
46 NO:5.  
48 <400> SEQUENCE: 2  
49 Gly Asn Ala Glu His Val Ala Ser Ala Val Glu Asn Ala Asn Arg Val  
50 1 5 10 15  
52 Asn Lys  
56 <210> SEQ ID NO: 3  
57 <211> LENGTH: 15  
58 <212> TYPE: PRT  
59 <213> ORGANISM: Carybdea rastonii  
61 <220> FEATURE:  
62 <223> OTHER INFORMATION: This amino acid residue sequence corresponds to  
63 amino acid residue positions 363-377 of SEQ ID  
64 NO:5.

ENTERED

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66 <400> SEQUENCE: 3  
 67 Met Ser Asp Gly Phe Tyr Thr Met Glu Asn Ser Asp Arg Arg Lys  
 68 1 5 10 15  
 71 <210> SEQ ID NO: 4  
 72 <211> LENGTH: 1610  
 73 <212> TYPE: DNA  
 74 <213> ORGANISM: Carybdea rastonii  
 76 <220> FEATURE:  
 77 <221> NAME/KEY: CDS  
 78 <222> LOCATION: (28)..(1380)  
 80 <220> FEATURE:  
 81 <221> NAME/KEY: protein\_bind  
 82 <222> LOCATION: (1381)..(1610)  
 84 <400> SEQUENCE: 4  
 85 gcacaaggcga cttggtaag gagcacc atg att ctg aaa cat ctt cct tgg ctc 54  
 86 Met Ile Leu Lys His Leu Pro Trp Leu  
 87 1 5  
 89 ttt att gtc ctt gca att act tct gca aaa cat ggc aaa cgc tct gat 102  
 90 Phe Ile Val Leu Ala Ile Thr Ser Ala Lys His Gly Lys Arg Ser Asp  
 91 10 15 20 25  
 93 gtc aat tct tta ctt act aag gta gaa act gcc tta aaa gaa gct tct 150  
 94 Val Asn Ser Leu Leu Thr Lys Val Glu Thr Ala Leu Lys Glu Ala Ser  
 95 30 35 40  
 97 ggt agc aac gag gct ctt gag gct tta gag ggc tta aaa gga gag 198  
 98 Gly Ser Asn Glu Ala Ala Leu Glu Ala Leu Glu Gly Leu Lys Gly Glu  
 99 45 50 55  
 101 atc cag aca aaa cca gac cga gtt gga caa gcc aca aaa atc ctt gga 246  
 102 Ile Gln Thr Lys Pro Asp Arg Val Gly Gln Ala Thr Lys Ile Leu Gly  
 103 60 65 70  
 105 tct gtc gga tca gct cta gga aaa tta aat tct gga gat gca acc aaa 294  
 106 Ser Val Gly Ser Ala Leu Gly Lys Leu Asn Ser Gly Asp Ala Thr Lys  
 107 75 80 85  
 109 atc att tct ggt tgc ctc gac att gtt gca gga att gca aca act ttt 342  
 110 Ile Ile Ser Gly Cys Leu Asp Ile Val Ala Gly Ile Ala Thr Thr Phe  
 111 90 95 100 105  
 113 gga ggc cct gtc ggg atg gga atc gga gcc gta gct tct ttt gtt tct 390  
 114 Gly Gly Pro Val Gly Met Gly Ile Gly Ala Val Ala Ser Phe Val Ser  
 115 110 115 120  
 117 tca att cta tca ttg ttt act gga agc tca gca aag aac tca gtt gct 438  
 118 Ser Ile Leu Ser Leu Phe Thr Gly Ser Ser Ala Lys Asn Ser Val Ala  
 119 125 130 135  
 121 gcc gtt att gat aga gct tta agc aag cat cgc gat gag gcc atc caa 486  
 122 Ala Val Ile Asp Arg Ala Leu Ser Lys His Arg Asp Glu Ala Ile Gln  
 123 140 145 150  
 125 aga cat gca gca ggt gcc aag aga gat ttt gct gaa tca tct gca ttc 534  
 126 Arg His Ala Ala Gly Ala Lys Arg Asp Phe Ala Glu Ser Ser Ala Phe  
 127 155 160 165  
 129 att cag gtc atg aaa cag cag tcc aat ctt aca gat agc gac cta agt 582  
 130 Ile Gln Val Met Lys Gln Gln Ser Asn Leu Thr Asp Ser Asp Leu Ser

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131	170	175	180	185	
133	atc att gca gcg aat gtt cct gtt tat aaa ttt agt aat ttt atc gga				630
134	Ile Ile Ala Ala Asn Val Pro Val Tyr Lys Phe Ser Asn Phe Ile Gly				
135	190	195	200		
137	cag ttg gag agc aga att tcc caa ggc gca gca act acc agt ctt agc				678
138	Gln Leu Glu Ser Arg Ile Ser Gln Gly Ala Ala Thr Thr Ser Leu Ser				
139	205	210	215		
141	gat gca aag aga gcc gtt gac ttc att ctg ctc tat tgt caa ctt gta				726
142	Asp Ala Lys Arg Ala Val Asp Phe Ile Leu Leu Tyr Cys Gln Leu Val				
143	220	225	230		
145	gtc atg aga gaa acc ttg ctg gtc gac ttg gct att ctc tac agg aaa				774
146	Val Met Arg Glu Thr Leu Leu Val Asp Leu Ala Ile Leu Tyr Arg Lys				
147	235	240	245		
149	gga aat gca gaa cac gtg gca agt gct gtg gaa aac gct aat agg gta				822
150	Gly Asn Ala Glu His Val Ala Ser Ala Val Glu Asn Ala Asn Arg Val				
151	250	255	260	265	
153	aac aaa gag cta gct gat acc cta gat ttt ctt cat aaa ttg att				870
154	Asn Lys Glu Leu Ala Ala Asp Thr Leu Asp Phe Leu His Lys Leu Ile				
155	270	275	280		
157	cct gaa caa gca ttg ata ggt gca gtt tat cat cca att tct gcc tct				918
158	Pro Glu Gln Ala Leu Ile Gly Ala Val Tyr His Pro Ile Ser Ala Ser				
159	285	290	295		
161	gaa act agc aaa gca ata tta aat tac acg aaa tac ttt gga gtt cca				966
162	Glu Thr Ser Lys Ala Ile Leu Asn Tyr Thr Lys Tyr Phe Gly Val Pro				
163	300	305	310		
165	gat gtt ccc cgt cct att gga aac cgc aga tac aaa ttt aca aat agt				1014
166	Asp Val Pro Arg Pro Ile Gly Asn Arg Arg Tyr Lys Phe Thr Asn Ser				
167	315	320	325		
169	tac tgg aat acc tac agt ata tgc agt gag gct tac atg gga aat tac				1062
170	Tyr Trp Asn Thr Tyr Ser Ile Cys Ser Glu Ala Tyr Met Gly Asn Tyr				
171	330	335	340	345	
173	atg ttc aga ggc tgt tct aac gtt cgg aat cca aat atc agg gta tcc				1110
174	Met Phe Arg Gly Cys Ser Asn Val Arg Asn Pro Asn Ile Arg Val Ser				
175	350	355	360		
177	aaa atg tct gat ggg ttt tac acc atg gag aat agc gat cgg agg aag				1158
178	Lys Met Ser Asp Gly Phe Tyr Thr Met Glu Asn Ser Asp Arg Arg Lys				
179	365	370	375		
181	ttg tat atc acc aag cat gac caa gga tgg gga tgg ggt act ttg gat				1206
182	Leu Tyr Ile Thr Lys His Asp Gln Gly Trp Gly Trp Gly Thr Leu Asp				
183	380	385	390		
185	gag gat cca ggt gac caa ggc cat atg agg ttc att cct ttg aga cat				1254
186	Glu Asp Pro Gly Asp Gln Gly His Met Arg Phe Ile Pro Leu Arg His				
187	395	400	405		
189	ggg aag tat atg gta agc tct aag agg tgg ccc aac tgg ttc atg tat				1302
190	Gly Lys Tyr Met Val Ser Ser Lys Arg Trp Pro Asn Trp Phe Met Tyr				
191	410	415	420	425	
193	atg gaa tca agt gcc agt ggc tac att cgc agc tgg gaa aat aat cca				1350
194	Met Glu Ser Ser Ala Ser Gly Tyr Ile Arg Ser Trp Glu Asn Asn Pro				
195	430	435	440		

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197 gga cct caa gga cat tgg agt ata aca taa ttaaaagagga atcaacaatg      1400
198 Gly Pro Gln Gly His Trp Ser Ile Thr
199          445          450
201 tcccaaaggc atacgaatat aagacatcaa acgaatgcag tacttaaagt gcacacttgt 1460
203 atttctacat aggatgtcgt catgaaaagtc cataaaccat ccagcgact aatttcatat 1520
205 taaacattaa tgtttcctta taatgcattt tcataaattc tctatttgta catttcaaga 1580
207 ggatatgttt gaaagaaaaca aaaaaaaaaa 1610
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 450
212 <212> TYPE: PRT
213 <213> ORGANISM: Carybdea rastonii
215 <400> SEQUENCE: 5
216 Met Ile Leu Lys His Leu Pro Trp Leu Phe Ile Val Leu Ala Ile Thr
217     1           5           10          15
219 Ser Ala Lys His Gly Lys Arg Ser Asp Val Asn Ser Leu Leu Thr Lys
220     20          25          30
222 Val Glu Thr Ala Leu Lys Glu Ala Ser Gly Ser Asn Glu Ala Ala Leu
223     35          40          45
225 Glu Ala Leu Glu Gly Leu Lys Gly Glu Ile Gln Thr Lys Pro Asp Arg
226     50          55          60
228 Val Gly Gln Ala Thr Lys Ile Leu Gly Ser Val Gly Ser Ala Leu Gly
229     65          70          75          80
231 Lys Leu Asn Ser Gly Asp Ala Thr Lys Ile Ile Ser Gly Cys Leu Asp
232     85          90          95
234 Ile Val Ala Gly Ile Ala Thr Thr Phe Gly Gly Pro Val Gly Met Gly
235     100         105         110
237 Ile Gly Ala Val Ala Ser Phe Val Ser Ser Ile Leu Ser Leu Phe Thr
238     115         120         125
240 Gly Ser Ser Ala Lys Asn Ser Val Ala Ala Val Ile Asp Arg Ala Leu
241     130         135         140
243 Ser Lys His Arg Asp Glu Ala Ile Gln Arg His Ala Ala Gly Ala Lys
244     145         150         155         160
246 Arg Asp Phe Ala Glu Ser Ser Ala Phe Ile Gln Val Met Lys Gln Gln
247     165         170         175
249 Ser Asn Leu Thr Asp Ser Asp Leu Ser Ile Ile Ala Ala Asn Val Pro
250     180         185         190
252 Val Tyr Lys Phe Ser Asn Phe Ile Gly Gln Leu Glu Ser Arg Ile Ser
253     195         200         205
255 Gln Gly Ala Ala Thr Thr Ser Leu Ser Asp Ala Lys Arg Ala Val Asp
256     210         215         220
258 Phe Ile Leu Leu Tyr Cys Gln Leu Val Val Met Arg Glu Thr Leu Leu
259     225         230         235         240
261 Val Asp Leu Ala Ile Leu Tyr Arg Lys Gly Asn Ala Glu His Val Ala
262     245         250         255
264 Ser Ala Val Glu Asn Ala Asn Arg Val Asn Lys Glu Leu Ala Ala Asp
265     260         265         270
267 Thr Leu Asp Phe Leu His Lys Leu Ile Pro Glu Gln Ala Leu Ile Gly
268     275         280         285
270 Ala Val Tyr His Pro Ile Ser Ala Ser Glu Thr Ser Lys Ala Ile Leu

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271      290          295          300
273 Asn Tyr Thr Lys Tyr Phe Gly Val Pro Asp Val Pro Arg Pro Ile Gly
274 305           310           315           320
276 Asn Arg Arg Tyr Lys Phe Thr Asn Ser Tyr Trp Asn Thr Tyr Ser Ile
277           325           330           335
279 Cys Ser Glu Ala Tyr Met Gly Asn Tyr Met Phe Arg Gly Cys Ser Asn
280           340           345           350
282 Val Arg Asn Pro Asn Ile Arg Val Ser Lys Met Ser Asp Gly Phe Tyr
283           355           360           365
285 Thr Met Glu Asn Ser Asp Arg Arg Lys Leu Tyr Ile Thr Lys His Asp
286           370           375           380
288 Gln Gly Trp Gly Trp Gly Thr Leu Asp Glu Asp Pro Gly Asp Gln Gly
289 385           390           395           400
291 His Met Arg Phe Ile Pro Leu Arg His Gly Lys Tyr Met Val Ser Ser
292           405           410           415
294 Lys Arg Trp Pro Asn Trp Phe Met Tyr Met Glu Ser Ser Ala Ser Gly
295           420           425           430
297 Tyr Ile Arg Ser Trp Glu Asn Asn Pro Gly Pro Gln Gly His Trp Ser
298           435           440           445
300 Ile Thr
301   450
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 19
306 <212> TYPE: DNA
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: Degenerate PCR
311 primer, 7-F, used in the cloning of the partial
312 cDNA of the hemolytic active protein of Carybdea
313 rastonii
315 <220> FEATURE:
316 <221> NAME/KEY: unsure
317 <222> LOCATION: (12)
318 <223> OTHER INFORMATION: n = inosine
320 <220> FEATURE:
321 <221> NAME/KEY: unsure
322 <222> LOCATION: (18)
323 <223> OTHER INFORMATION: n = inosine
325 <400> SEQUENCE: 6
326 garathcara cnaarcng                                19
329 <210> SEQ ID NO: 7
330 <211> LENGTH: 19
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <221> NAME/KEY: unsure
336 <222> LOCATION: (2)
337 <223> OTHER INFORMATION: n = inosine
339 <220> FEATURE:

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/647,522

DATE: 03/18/2002  
TIME: 15:20:40

Input Set : A:\Nagai h.app  
Output Set: N:\CRF3\03182002\I647522.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13